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ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC	60
ATGTGCTTT TAAATTGGCC TGGTGACCC GCCCCACTGG TGTAAGAAGA GAACCGGCCA	120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGGAGC ACTGCTTCAG CAACAAAGCC	180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC	231
Met Ala Thr Ser Trp Gly Ala Val Phe	
1 5	
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG	279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln	
10 15 20 25	
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT	327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn	
30 35 40	
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT	375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr	
45 50 55	
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG	423
Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln	
60 65 70	
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT	471
Leu Pro Phe Leu Glu Ile Phe Asp Ser Val Lys Pro Gly Leu	
75 80 85	
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu	
90 95 100 105	
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Ile Phe Lys Asn	
140 145 150	
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	
170 175 180 185	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	
190 195 200	
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	
205 210 215	
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	
220 225 230	

Fig. 1

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TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gin Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Val Arg Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

FIG. 1 (cont'd.)

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TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCAC	AGACTGTAAA	TCTTTGGGA	1749
TTCTTGTAC	AGAGTCTGC	AAAGGAAAAA	AGAGAAAAGG	TTTGGAACTC	CATGCTAGAT	1809
TGCGACTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAAAT	CTCGTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTG	TTATAAGCTG	ATTTACTGAA	ATCCCATAAC	1929
CCATCAATGC	TGTTAATT	TTCTTCCTA	CCCTTATTAC	ATCCCTACC	CTAAAAGCCT	1989
GGGGGAATAA	CCTGGTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAA						2119

FIG. 1 (cont'd.)

peaNTPase	1	----HELEIKLTTFPLYSMVKATSSQVQGNMULTSRDPFPGCPISSVAVVFDAGSTGSR
potapyrase	1	MLNQNSHFIPIFLAMPLVLELSLSKVNNAQMPUREHILKESSE..HVAVHFDAGSTGSR
mNTPase	1	WATSGWATPMNIAACWGSTVFFYRQQCTMFZGFLGSNCPINVSGAGTNGIMFDAGSTGSR
yGDPase	1	KSPEDHITMPYDPERGMLQDGKPEQNLADAVKSQTSQTCSEBHNVIMIDAGSTGSR
peaNTPase	57	IHVYBFAQNLQLLHIGKGVEYVMAITPGLSSYATPPEQAAKSLIPPLLEQAEVVPPDLOP
potapyrase	59	WVHVRPDEKLCLLPLIGNNIIPYPMATEPGLSSYALDEKAAANSLEPLHCAEGVVIQLOS
mNTPase	61	IEVYTGWOKTAGOLEFLCCEHIFDPMVNPGLSPLVVEPKOGAEVYQELBEVANSDSIRSHW
yGDPase	61	VHMYKEDVCTG..PPTLDEPKPMEPGLSSEEDTOSVGAANSQPLKVAANNYVPIKANS
peaNTPase	117	CFPVRLGATAGRLRLNGDASEKILQSVRDQHISNRSTF..NVPDVAISIMDGTQEGSYLWV
potapyrase	119	TPPLQGATAGRLMKGDAEAKILQSVRDQHISNRSTF..HSKPOWVHIMDGTQEGSYLWV
mNTPase	121	CFPVRLGATAGRLRLPEQVQALQVLLVETVSKAN..SPF..LVPDOSVSIMDGSYEGFLANV
yGDPase	119	CFPVRLGATAGRLLLGDAKSILSVADELEKDYPPFVYEDGVSIMGCDIECVKAMT
peaNTPase	176	VNVIALGHNLRHRYTN..IYGVLIDLGGGSVQMAVAVSKAKAKNAPKWDGDPYTKKVVHKG
potapyrase	178	INYLLCNCNLMDKGS..ATATDHLGGGSVQMAVAVSKAKAKNAPKWDGDPYTKKVVHKG
mNTPase	179	VNLLELGCGLEEGQE..IYGVLIDLGGGSVQMAVAVSKAKAKNAPKWDGDPYTKKVVHKG
yGDPase	179	TNYLIGNEGANGRKLPAAMVLLGGGSTQVVEP..TDPINZKMDGKHKZ..DGGTGD
peaNTPase	234	IPICHLVHSYLDPGRASRAEILN..
potapyrase	235	KDMLVYHSYLNIGQLAGRAEIPKA..
mNTPase	232	STZALYTHSYLGEGLKAARLATEQ..
yGDPase	234	ENPLVYQSHLGWGLNEGRNKNVNSVLVENDALKGKILKGDNTRKREGLSSPCIPFKVMDATN
peaNTPase	276	TVSGEEPKATAATYTSGN..NQKXCNTRIRALKHNPFCYQ..NCTFGGIWNNGGGN..
potapyrase	277	SYGQVDMKVKNDKKG..SWKRCRRLTRALHNPFCYQ..NCTFGGIWNNGGGN..
mNTPase	270	KCIPRMLBAZWIFCCV..KCYIGGCRQKGMGFPFCYQ..LAVVQGKDRQPEEV..
yGDPase	294	EKVTLESKETTIDFIGPDEPSGAQCRPDTDEIENKDAQGQSPFCSENGVHQPSLVHTFK
peaNTPase	328	GOKNIIASSPFLYLPDTGKVDPSGPSTPN..MLPDPDIEITKAKEACALNEADAKS..TFLDKE
potapyrase	329	GOKNIIASSPFLYLPDTGKVDPSGPSTPN..MLPDPDIEITKAKEACALNEADAKS..TFLDKE
mNTPase	322	GS..IYAPPSVYDRAADTFLHIZPE..KGVVLLVZDPERKAREVGH..NGQSFSCS..
yGDPase	354	ESNDIYLPSVYDRAADTFLHIZPE..KGVVLLVZDPERKAREVGH..NGQSFSCS..
peaNTPase	388	IVASVYCMDLILYQVLLVDPGFLDPLKIKTSGKPLIEYQHAIWAAWPLGNAVKAISALPK
potapyrase	389	NH..PYLCMDLILYQVLLVDPGFLDPLKIKTSGKPLIEYQHAIWAAWPLGNAVKAISALPK
mNTPase	374	..RCLMDLITVIALLHDGEPAZERPLAHLKRESEQRDWLGQHBLSCAPVSGHHOLR
yGDPase	411	ESDSHFCGLDMSKQVSLLTGQDPLQOREHRTGKIANKE..IGCQGCAASIPFLKADNN
peaNTPase	448	PERCHMYFV..
potapyrase	448	MIRVASH..
mNTPase	430	PSSTSPACISEPPVFSQEGVDSETPSDSLGSKAWEPTR..
yGDPase	467	CKEKOZA..

FIG. 2

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ACR I

CD39	1	KEKLVLYLQGK	5	YVY	9	AVVLLPPLP	13	EV	17	EV	21	EV	25	EV	29	EV	33	EV	37	EV	41	EV	45	EV	49	EV	53	EV	57	EV	61	EV	65	EV	69	EV	73	EV	77	EV	81	EV	85	EV	89	EV	93	EV	97	EV	101	EV	105	EV	109	EV	113	EV	117	EV	121	EV	125	EV	129	EV	133	EV	137	EV	141	EV	145	EV	149	EV	153	EV	157	EV	161	EV	165	EV	169	EV	173	EV	177	EV	181	EV	185	EV	189	EV	193	EV	197	EV	201	EV	205	EV	209	EV	213	EV	217	EV	221	EV	225	EV	229	EV	233	EV	237	EV	241	EV	245	EV	249	EV	253	EV	257	EV	261	EV	265	EV	269	EV	273	EV	277	EV	281	EV	285	EV	289	EV	293	EV	297	EV	301	EV	305	EV	309	EV	313	EV	317	EV	321	EV	325	EV	329	EV	333	EV	337	EV	341	EV	345	EV	349	EV	353	EV	357	EV	361	EV	365	EV	369	EV	373	EV	377	EV	381	EV	385	EV	389	EV	393	EV	397	EV	401	EV	405	EV	409	EV	413	EV	417	EV	421	EV	425	EV	429	EV	433	EV	437	EV	441	EV	445	EV	449	EV	453	EV	457	EV	461	EV	465	EV	469	EV	473	EV	477	EV	481	EV	485	EV	489	EV	493	EV	497	EV	501	EV	505	EV	509	EV	513	EV	517	EV	521	EV	525	EV	529	EV	533	EV	537	EV	541	EV	545	EV	549	EV	553	EV	557	EV	561	EV	565	EV	569	EV	573	EV	577	EV	581	EV	585	EV	589	EV	593	EV	597	EV	601	EV	605	EV	609	EV	613	EV	617	EV	621	EV	625	EV	629	EV	633	EV	637	EV	641	EV	645	EV	649	EV	653	EV	657	EV	661	EV	665	EV	669	EV	673	EV	677	EV	681	EV	685	EV	689	EV	693	EV	697	EV	701	EV	705	EV	709	EV	713	EV	717	EV	721	EV	725	EV	729	EV	733	EV	737	EV	741	EV	745	EV	749	EV	753	EV	757	EV	761	EV	765	EV	769	EV	773	EV	777	EV	781	EV	785	EV	789	EV	793	EV	797	EV	801	EV	805	EV	809	EV	813	EV	817	EV	821	EV	825	EV	829	EV	833	EV	837	EV	841	EV	845	EV	849	EV	853	EV	857	EV	861	EV	865	EV	869	EV	873	EV	877	EV	881	EV	885	EV	889	EV	893	EV	897	EV	901	EV	905	EV	909	EV	913	EV	917	EV	921	EV	925	EV	929	EV	933	EV	937	EV	941	EV	945	EV	949	EV	953	EV	957	EV	961	EV	965	EV	969	EV	973	EV	977	EV	981	EV	985	EV	989	EV	993	EV	997	EV	1001	EV	1005	EV	1009	EV	1013	EV	1017	EV	1021	EV	1025	EV	1029	EV	1033	EV	1037	EV	1041	EV	1045	EV	1049	EV	1053	EV	1057	EV	1061	EV	1065	EV	1069	EV	1073	EV	1077	EV	1081	EV	1085	EV	1089	EV	1093	EV	1097	EV	1101	EV	1105	EV	1109	EV	1113	EV	1117	EV	1121	EV	1125	EV	1129	EV	1133	EV	1137	EV	1141	EV	1145	EV	1149	EV	1153	EV	1157	EV	1161	EV	1165	EV	1169	EV	1173	EV	1177	EV	1181	EV	1185	EV	1189	EV	1193	EV	1197	EV	1201	EV	1205	EV	1209	EV	1213	EV	1217	EV	1221	EV	1225	EV	1229	EV	1233	EV	1237	EV	1241	EV	1245	EV	1249	EV	1253	EV	1257	EV	1261	EV	1265	EV	1269	EV	1273	EV	1277	EV	1281	EV	1285	EV	1289	EV	1293	EV	1297	EV	1301	EV	1305	EV	1309	EV	1313	EV	1317	EV	1321	EV	1325	EV	1329	EV	1333	EV	1337	EV	1341	EV	1345	EV	1349	EV	1353	EV	1357	EV	1361	EV	1365	EV	1369	EV	1373	EV	1377	EV	1381	EV	1385	EV	1389	EV	1393	EV	1397	EV	1401	EV	1405	EV	1409	EV	1413	EV	1417	EV	1421	EV	1425	EV	1429	EV	1433	EV	1437	EV	1441	EV	1445	EV	1449	EV	1453	EV	1457	EV	1461	EV	1465	EV	1469	EV	1473	EV	1477	EV	1481	EV	1485	EV	1489	EV	1493	EV	1497	EV	1501	EV	1505	EV	1509	EV	1513	EV	1517	EV	1521	EV	1525	EV	1529	EV	1533	EV	1537	EV	1541	EV	1545	EV	1549	EV	1553	EV	1557	EV	1561	EV	1565	EV	1569	EV	1573	EV	1577	EV	1581	EV	1585	EV	1589	EV	1593	EV	1597	EV	1601	EV	1605	EV	1609	EV	1613	EV	1617	EV	1621	EV	1625	EV	1629	EV	1633	EV	1637	EV	1641	EV	1645	EV	1649	EV	1653	EV	1657	EV	1661	EV	1665	EV	1669	EV	1673	EV	1677	EV	1681	EV	1685	EV	1689	EV	1693	EV	1697	EV	1701	EV	1705	EV	1709	EV	1713	EV	1717	EV	1721	EV	1725	EV	1729	EV	1733	EV	1737	EV	1741	EV	1745	EV	1749	EV	1753	EV	1757	EV	1761	EV	1765	EV	1769	EV	1773	EV	1777	EV	1781	EV	1785	EV	1789	EV	1793	EV	1797	EV	1801	EV	1805	EV	1809	EV	1813	EV	1817	EV	1821	EV	1825	EV	1829	EV	1833	EV	1837	EV	1841	EV	1845	EV	1849	EV	1853	EV	1857	EV	1861	EV	1865	EV	1869	EV	1873	EV	1877	EV	1881	EV	1885	EV	1889	EV	1893	EV	1897	EV	1901	EV	1905	EV	1909	EV	1913	EV	1917	EV	1921	EV	1925	EV	1929	EV	1933	EV	1937	EV	1941	EV	1945	EV	1949	EV	1953	EV	1957	EV	1961	EV	1965	EV	1969	EV	1973	EV	1977	EV	1981	EV	1985	EV	1989	EV	1993	EV	1997	EV	2001	EV	2005	EV	2009	EV	2013	EV	2017	EV	2021	EV	2025	EV	2029	EV	2033	EV	2037	EV	2041	EV	2045	EV	2049	EV	2053	EV	2057	EV	2061	EV	2065	EV	2069	EV	2073	EV	2077	EV	2081	EV	2085	EV	2089	EV	2093	EV	2097	EV	2101	EV	2105	EV	2109	EV	2113	EV	2117	EV	2121	EV	2125	EV	2129	EV	2133	EV	2137	EV	2141	EV	2145	EV	2149	EV	2153	EV	2157	EV	2161	EV	2165	EV	2169	EV	2173	EV	2177	EV	2181	EV	2185	EV	2189	EV	2193	EV	2197	EV	2201	EV	2205	EV	2209	EV	2213	EV	2217	EV	2221	EV	2225	EV	2229	EV	2233	EV	2237	EV	2241	EV	2245	EV	2249	EV	2253	EV	2257	EV	2261	EV	2265	EV	2269	EV	2273	EV	2277	EV	2281	EV	2285	EV	2289	EV	2293	EV	2297	EV	2301	EV	2305	EV	2309	EV	2313	EV	2317	EV	2321	EV	2325	EV	2329	EV	2333	EV	2337	EV	2341	EV	2345	EV	2349	EV	2353	EV	2357	EV	2361	EV	2365	EV	2369	EV	2373	EV	2377	EV	2381	EV	2385	EV	2389	EV	2393	EV	2397	EV	2401	EV	2405	EV	2409	EV	2413	EV	2417	EV	2421	EV	2425	EV	2429	EV	2433	EV	2437	EV	2441	EV	2445	EV	2449	EV	2453	EV	2457	EV	2461	EV	2465	EV	2469	EV	2473	EV	2477	EV	2481	EV	2485	EV	2489	EV	2493	EV	2497	EV	2501	EV	2505	EV	2509	EV	2513	EV	2517	EV	2521	EV	2525	EV	2529	EV	2533	EV	2537	EV	2541	EV	2545	EV	2549	EV	2553	EV	2557	EV	2561	EV	2565	EV	2569	EV	2573	EV	2577	EV	2581	EV	2585	EV	2589	EV	2593	EV	2597	EV	2601	EV	2605	EV	2609	EV	2613	EV	2617	EV	2621	EV	2625	EV	2629	EV	2633	EV	2637	EV	2641	EV	2645	EV	2649	EV	2653	EV	2657	EV	2661	EV	2665	EV	2669	EV	2673	EV	2677	EV	2681	EV	2685	EV	2689	EV	2693	EV	2697	EV	2701	EV	2705	EV	2709	EV	2713	EV	2717	EV	2721	EV	2725	EV	2729	EV	2733	EV	2737	EV	2741	EV	2745	EV	2749	EV	2753	EV	2757	EV	2761	EV	2765	EV	2769	EV	2773	EV	2777	EV	2781	EV	2785	EV	2789	EV	2793	EV	2797	EV	2801	EV	2805	EV	2809	EV	2813	EV	2817	EV	2821	EV	2825	EV	2829	EV	2833	EV	2837	EV	2841	EV	2845	EV	2849	EV	2853	EV	2857	EV	2861	EV	2865	EV	2869	EV	2873	EV	2877	EV	2881	EV	2885	EV	2889	EV	2893	EV	2897	EV	2901	EV	2905	EV	2909	EV	2913	EV	2917	EV	2921	EV	2925	EV	2929	EV	2933	EV	2937	EV	2941	EV	2945	EV	2949	EV	2953	EV	2957	EV	2961	EV	2965	EV	2969	EV	2973	EV	2977	EV	2981	EV	2985	EV	2989	EV	2993	EV	2997	EV	3001	EV	3005	EV	3009	EV	3013	EV	3017	EV	3021	EV	3025	EV	3029	EV	3033	EV	3037	EV	3041	EV	3045	EV	3049	EV	3053	EV	3057	EV	3061	EV	3065	EV	3069	EV	3073	EV	3077	EV	3081	EV	3085	EV	3089	EV	3093	EV	3097	EV	3101	EV	3105	EV	3109	EV	3113	EV	3117	EV	3121	EV	3125	EV	3129	EV	3133	EV	3137	EV	3141	EV	3145	EV	3149	EV	3153	EV	3157	EV	3161	EV	3165	EV	3169	EV	3173	EV	3177	EV	3181	EV	3185	EV	3189	EV	3193	EV	3197	EV	3201	EV	3205	EV	3209	EV	3213	EV	3217	EV	3221	EV	3225	EV	3229	EV	3233	EV	3237	EV	3241	EV	3245	EV	3249	EV	3253	EV	3257	EV	3261	EV	3265	EV	3269	EV	3273	EV	3277	EV	3281	EV	3285	EV	3289	EV	3293	EV	3297	EV	3301	EV	3305	EV	3309	EV	3313	EV	3317	EV	3321	EV	3325	EV	3329	EV	3333	EV	
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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCAA	60
AAGACCGGCT GCCGCGCTGCT CCCCGGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
GCGCGGTGCA TGGATGGC TATGTGATG AAAAAAGGTA TCCGTTATGA AACTCCAGA	180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCTCT CGTGCCTGGA CGTGAATTCA TCTTGAGGAG CCACAGCACA GGCCGTGCTG GCACCTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC 1697 1757 1817	

FIG. 4 (cont'd.)

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AATGCCACCT	GTCTGCCCTGG	GCTCCAAGTG	GGCAGGGACCA	GGACAGAAC	ACAGGCACAC	1877
ACTGAGGGGG	CACTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTCCATGTCC	CTGCGATGGG	AGTCTTGTCT	CCCAAGCTGT	CAGTTTCCTC	1997
CCCAGGGCAG	ACCTCCCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTCAGGCT	GTCTGGCTG	2057
CTCTGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGGAC	AGTAGGTCTG	GGCGGCACCA	2117
CTGGGAACTC	TGGACTTGAG	TGTGTTGCT	CTTCCTTGGG	TATGAATGTG	TGAGTTCAACC	2177
CAGAGGCCTG	CTCTCCTCAC	ACATTGTGTG	GTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTCAG	GGAGTCTCCC	AGCATGGCG	GATGCCGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAA		2762

Fig. 4 (cont'd)

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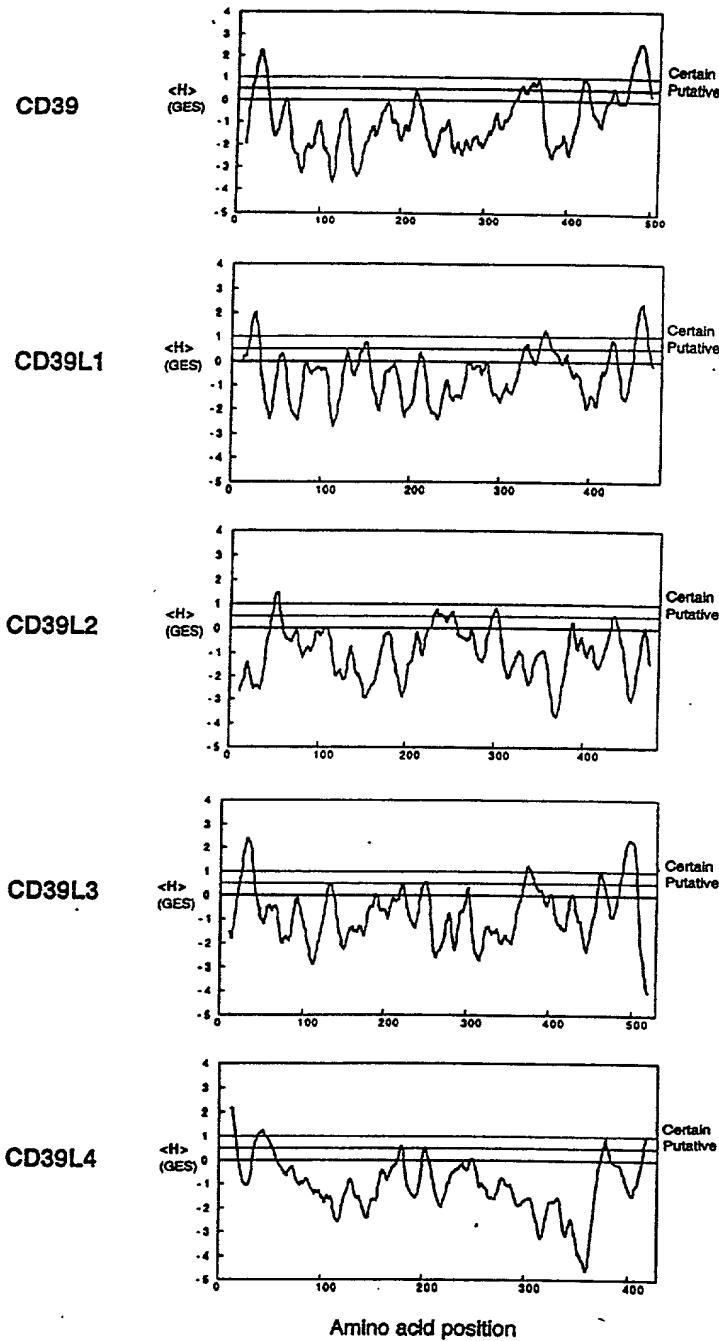


FIG. 5

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ACCCACCGCGT CTGGCCGCGG GCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT Met Phe Thr Val Leu Thr Arg Gln Pro Cys	60 112
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	160
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	208
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	256
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	304
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	352
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	400
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	448
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	496
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	544
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	592
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	640
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	688
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	736
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	784
220 225 230	

Fig. 6

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ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

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CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTC AAGCAGCTCC TGGAGTCCAA TGGC	1703
Asp His Ala Val Asp Ser Asp	
525	
TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAAGAAA	1763
TACAACTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC	1823
AGCACCTCTT GAGGCATCCC TTGGCTATTG TGTCATATT GTCTTCAGA GACCTCACTA	1883
CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTG AGGCTCTTA	1943
TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AAGAAGTATC AGTTTAATGT TGAAGAATTG	2003
ACCTCAGGGC TCAGTTCCA TTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA	2063
AGCATTTCGC CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT	2123
TTCTTGAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG	2183
GGAGAAAGACT TACTCCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA	2243
TCCCAGAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG	2303
GAATTCCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTGTC ATCATCCTCA	2363
TCTCACCAT TGTATTGCTAT GCGCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT	2423
GCATTCAGA TTTTACTGCC TTGGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTCCATT	2483
GTTATCATGG TGTATATATT TTGTCACCA TTCCCACAAG TATACTGT GTTGTCTAG	2543
AACGAACATC CTACTCTATG ATTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT	2603
GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC	2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA	2723
TTATTCATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTGA	2783
AAAAAAAAA AAAA	2797

FIG. 6 (cont'd.)

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GGCGCGCGGT	TTTCCTTGT	CCTGGTCAAC	AAAGAAATGT	GGAGTGTCTT	GGCTGAATCC	60
TCATACAGAC	AAGATCATTA	TGGTGTGTT	AGGTAGGACT	TGTATCCAGA	TGTAAGGTTG	120
AAAAAGTGAT	ATAATAAAGG	ACCAAGGAG	AAAATTCAAGA	AGGAAAGAAA	AAATTGCCTC	180
TGCAGGTGTG	CGAGCAGGAT	TGCTTCTGCA	ACAAAAGCCT	CCACCCAGCC	ACATCTTGGG	240
AAAAGA ATG	GCC ACT	TCT TGG GGC	ACA GTC TTT	TTC ATG CTG	GTG GTA	288
Met Ala Thr Ser	Trp Gly Thr	Val Phe	Phe Met	Leu Val	Val	
1	5		10			
TCC TGT GTT	TGC AGC GCT	TCC CAC AGG AAC	CAG CAG ACT	TGG TTT		336
Ser Cys Val	Cys Ser Ala Val	Ser His Arg	Asn Gln Gln	Thr Trp Phe		
15	20	25	30			
GAG GGT ATC	TTC CTG TCT	TCC ATG TGC	CCC ATC AAT	GTC AGC GCC AGC		384
Glu Gly Ile	Phe Leu Ser	Ser Met Cys	Pro Ile Asn	Val Ser Ala Ser		
35	40	45				
ACC TTG TAT	GGA ATT ATG	TTT GAT GCA	GGG AGC ACT	GGA ACT CGA ATT		432
Thr Leu Tyr	Gly Ile Met	Phe Asp Ala	Gly Ser Thr	Gly Thr Arg Ile		
50	55	60				
CAT GTT TAC ACC	TTT GTG CAG	AAA ATG CCA GGA	CAG CTT CCA ATT CTA			480
His Val Tyr	Thr Phe Val	Gln Lys Met Pro	Gly Gln Leu	Pro Ile Leu		
65	70	75				
GAA GGG GAA	GTT TTT GAT TCT	GTG AAG CCA GGA	CTT TCT GCT TTT GTA			528
Glu Gly Glu Val	Phe Asp Ser Val	Lys Pro Gly	Leu Ser Ala	Phe Val		
80	85	90				
GAT CAA CCT AAG	CAG GGT GCT	GAG ACC GTT CAA	GGG CTC TTA GAG GTG			576
Asp Gln Pro	Lys Gln Gly	Ala Glu Thr Val	Gln Gly Leu	Leu Glu Val		
95	100	105	110			
GCC AAA GAC TCA	ATC CCC CGA AGT	CAC TGG AAA AAG	ACC CCA GTG GTC			624
Ala Lys Asp Ser	Ile Pro Arg Ser	His Trp Lys	Lys Thr Pro	Val Val		
115	120	125				
CTA AAG GCA	ACA GCA GGA	CTA CGC TTA CTG	CCA GAA CAC AAA	GCC AAG		672
Leu Lys Ala Thr	Ala Gly Leu Arg	Leu Pro Glu His	Lys Ala Lys			
130	135	140				
GCT CTG CTC	TTT GAG GTC	AAG GAG ATC	TTC AGG AAG TCA	CCT TTC CTG		720
Ala Leu Leu	Phe Glu Val	Lys Glu Ile	Phe Arg Lys	Ser Pro Phe	Leu	
145	150	155				
GTA CCA AAG	GGC AGT GTT	AGC ATC ATG	GAT GGA TCC GAC	GAA GGC ATA		768
Val Pro Lys	Gly Ser Val	Ile Met Asp	Gly Ser Asp	Glu Gly Ile		
160	165	170				
TTA GCT TGG	GTT ACT GTG	AAT TTT CTG	ACA GGT CAG CTG	CAT GGC CAC		816
Leu Ala Trp	Val Thr Val	Asn Phe	Leu Thr	Gly Gln Leu	His Gly His	
175	180	185	190			
AGA CAG GAG	ACT GTG GGG	ACC TTG GAC	CTA GGG GGA	GCC TCC ACC CAA		864
Arg Gln Glu	Thr Val Gly	Thr Leu Asp	Leu Gly	Gly Ala Ser	Thr Gln	
195	200	205				
ATC ACG TTC	CTG CCC CAG	TTT GAG AAA	ACT CTG GAA CAA	ACT CCT AGG		912
Ile Thr Phe	Leu Pro Gln	Phe Glu	Lys Thr	Leu Glu Gln	Thr Pro Arg	
210	215	220				
GGC TAC CTC	ACT TCC TTT GAG	ATG TTT AAC AGC	ACT TAT AAG	CTC TAT		960
Gly Tyr Leu	Thr Ser Phe	Glu Met Phe	Asn Ser	Thr Tyr	Lys Leu Tyr	
225	230	235				

FIG. 7

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ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu 335 340 345 350	1296
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 355 360 365	1344
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 370 375 380	1392
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Ala Asp Ser Thr Val 385 390 395	1440
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 400 405 410	1488
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 415 420 425	1539
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG TTCTGAACT AGTCTGGAC ATCCCTGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT TACACATCTA ATGTGAAC TGCGCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA TCACAGAGAG CCCCCTGAGC CAAAAAGAT AGTTTTGGAA CTAAACCTTG GAGTGAAGAGC CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATT CAACCCCTTG AGTGCTCAT TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGTTAAACTG ACTTATTGCA ATCCCAAGAC CCATCAATAT CAGTATTTT TTCTCCCTA TACAGTGCCC TGCCCACCT TATCTGCACC CACCTCCCC GAAAAAGAGA GAAAAAAA AAAAAAAA	1599 1659 1719 1779 1839 1899 1959 1998

FIG. 7 (cont'd.)

Fig. 8.

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peaGDP	1	-----	-----	-----
potapyrase	1	-----	-----	-----
CD39L2	1	MKKGIRYETSRKTSTTIFOOPQKGPWOTRMKKEHNEGSLRVAVVYXPGLCVQVFY	Y	Y
CD39L4	1	-----	-----	-----
dNTPase	1	-----	MKYETL	TDEKPFRMGS
yGDPase	1	-----	GSPHASSGGNNRPSGH	-----
ACR I				
peaGDP	2	ELVLLKLTTFPESPLIASSQVLENH	LT	-----
potapyrase	6	SFIFPFL	-----	-----
CD39L2	61	KMTERATLQAFES	TR	-----
CD39L4	61	TPGARIGEOA	-----	-----
dNTPase	7	TEFT	-----	-----
yGDPase	37	TEFTLAVECVCSAVERHNOQFEGI	-----	-----
	5	RISFLCILISVILBLVFGFVERHASP	-----	-----
	5	PLRILSKFGYISRVOYAA	-----	-----
	5	DISILPNDPEFGTLDQSK	-----	-----
	5	EQDTPELADA	-----	-----
	5	KSQ	-----	-----
	5	SQTCSEEH	-----	-----
	5	YVIE	-----	-----
	5	DAGSTGSRVAY	-----	-----
ACR II				
peaGDP	61	EFNOMEDLHLIGKG	EV	-----
potapyrase	63	WFFHKLCLLPIGHN	EV	-----
CD39L2	119	PFETRPTDTH	TF	-----
CD39L4	66	TFVQNL	-----	-----
dNTPase	96	TFVQNL	-----	-----
yGDPase	65	KFIRSFIDMKLVLV	Y	-----
	5	ELFKERAKPGLSS	-----	-----
	5	ADPAPAHHS	-----	-----
	5	LLLDEAFY	-----	-----
	5	PFCHRSSTP	-----	-----
	5	KFV	-----	-----
	5	ACTSPFLLDKEDFM	-----	-----
	5	EPGLSS	-----	-----
	5	DTDSVCAAHSL	-----	-----
	5	PLLNKAM	-----	-----
	5	YVPIKANSC	-----	-----
ACR III				
peaGDP	121	RGATAGLRLLLNGDA	-----	-----
potapyrase	123	AEKILQEVRLD	-----	-----
CD39L2	178	AEKILQEVRLD	-----	-----
CD39L4	126	AEKILQEVRLD	-----	-----
dNTPase	156	AEKILQEVRLD	-----	-----
yGDPase	123	AEKATAGLRLLLGDA	-----	-----
ACR IV				
peaGDP	180	LGNLGKLYTK	-----	-----
potapyrase	182	LGNLGKLYKS	-----	-----
CD39L2	236	TGGLKTPGGS	-----	-----
CD39L4	184	TGGLKTPGGS	-----	-----
dNTPase	214	TGGLKTPGGS	-----	-----
yGDPase	183	TGGLKTPGGS	-----	-----
ACR V				
peaGDP	238	LYVHSYLFGRGAPRACILNLTPE	-----	-----
potapyrase	239	LYVHSYLFGRGAPRACILNLTPE	-----	-----
CD39L2	289	LYVHSYLFGRGAPRACILNLTPE	-----	-----
CD39L4	237	LYVHSYLFGRGAPRACILNLTPE	-----	-----
dNTPase	264	LYVHSYLFGRGAPRACILNLTPE	-----	-----
yGDPase	238	LYVHSYLFGRGAPRACILNLTPE	-----	-----
ACR VI				
peaGDP	276	TYVCGV	-----	-----
potapyrase	277	TYVCGV	-----	-----
CD39L2	335	TYVCGV	-----	-----
CD39L4	282	TYVCGV	-----	-----
dNTPase	308	TYVCGV	-----	-----
yGDPase	298	TYVCGV	-----	-----
ACR VII				
peaGDP	332	TYVCGV	-----	-----
potapyrase	333	TYVCGV	-----	-----
CD39L2	379	TYVCGV	-----	-----
CD39L4	326	TYVCGV	-----	-----
dNTPase	360	TYVCGV	-----	-----
yGDPase	358	TYVCGV	-----	-----
ACR VIII				
peaGDP	392	TYVCGV	-----	-----
potapyrase	392	TYVCGV	-----	-----
CD39L2	428	TYVCGV	-----	-----
CD39L4	375	TYVCGV	-----	-----
dNTPase	406	TYVCGV	-----	-----
yGDPase	415	TYVCGV	-----	-----
ACR IX				
peaGDP	452	MYFV	-----	-----
potapyrase	452	ASV	-----	-----
CD39L2	483	ASV	-----	-----
CD39L4	429	---	-----	-----
dNTPase	462	---	-----	-----
yGDPase	471	QSM	-----	-----

Fig. 9